

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, YI  
SU, KUI  
LI, HAODONG
- (ii) TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
(B) STREET: 9410 KEY WEST AVENUE  
(C) CITY: ROCKVILLE  
(D) STATE: MARYLAND  
(E) COUNTRY: USA  
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE: 20-MAR-1997  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Brookes, Anders, A.  
(B) REGISTRATION NUMBER: 36,373  
(C) REFERENCE/DOCKET NUMBER: PF270
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 301-309-8504  
(B) TELEFAX: 301-309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide

(B) LOCATION: 72..131

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 132..740

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 72..740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGGGC GACTTCGCGG GACCGTGGCG CATGTTTCCT GGGAGTTACT GATCATCTTC 60  
TTTGAAGAAA C ATG AAG TTA CAC TAT GTT GCT GTG CTT ACT CTA GCC ATC 110  
Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile  
-20 -15 -10  
CTG ATG TTC CTG ACA TGG CTT CCA GAA TCA CTG AGC TGT AAC AAA GCA 158  
Leu Met Phe Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala  
-5 1 5  
CTC TGT GCT AGT GAT GTG AGC AAA TGC CTC ATT CAG GAG CTC TGC CAG 206  
Leu Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln  
10 15 20 25  
TGC CGG CCG GGA GAA GGC AAT TGC TCC TGC TGT AAG GAG TGC ATG CTG 254  
Cys Arg Pro Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu  
30 35 40  
TGT CTT GGG GCC CTT TGG GAC GAG TGC TGT GAC TGT GTT GGT ATG TGT 302  
Cys Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys  
45 50 55  
AAT CCT CGA AAT TAT AGT GAC ACA CCT CCA ACT TCA AAG AGC ACA GTG 350  
Asn Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val  
60 65 70  
GAG GAG CTG CAT GAA CCG ATC CCT TCT CTC TTC CGG GCA CTC ACA GAA 398  
Glu Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu  
75 80 85  
GGA GAT ACT CAG TTG AAT TGG AAC ATC GTT TCT TTC CCT GTT GCA GAA 446  
Gly Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu  
90 95 100 105  
GAA CTT TCA CAT CAT GAG AAT CTG GTT TCA TTT TTA GAA ACT GTG AAC 494  
Glu Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn  
110 115 120  
CAG CCA CAC CAC CAG AAT GTG TCT GTC CCC AGC AAT AAT GTT CAC GCG 542  
Gln Pro His His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala  
125 130 135

CCT TAT TCC AGT GAC AAA GAA CAC ATG TGT ACT GTG GTT TAT TTT GAT	590
Pro Tyr Ser Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp	
140 145 150	
GAC TGC ATG TCC ATA CAT CAG TGT AAA ATA TCC TGT GAG TCC ATG GGA	638
Asp Cys Met Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly	
155 160 165	
GCA TCC AAA TAT CGC TGG TTT CAT AAT GCC TGC TGC GAG TGC ATT GGT	686
Ala Ser Lys Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly	
170 175 180 185	
CCA GAA TGT ATT GAC TAT GGT AGT AAA ACT GTC AAA TGT ATG AAC TGC	734
Pro Glu Cys Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys	
190 195 200	
ATG TTT TAAAGAAGAC AAATGCAAAC CAAAGCAACT TAGTAAAATA	780
Met Phe	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile Leu Met Phe	
-20 -15 -10 -5	
Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala Leu Cys Ala	
1 5 10	
Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro	
15 20 25	
Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu Cys Leu Gly	
30 35 40	
Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg	
45 50 55 60	
Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu	
65 70 75	
His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr	
80 85 90	
Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser	
95 100 105	

His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Pro His  
 110 115 120

His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Tyr Ser  
 125 130 135 140

Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met  
 145 150 155

Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys  
 160 165 170

Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys  
 175 180 185

Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe  
 190 195 200

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACGGATCC AGCTGTAACA AAGCACTCTG TG

32

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCAAGCTTT TAAACATGC AGTTCATACA TTTGAC

36

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATAGGATCC GCCATCATGA AGTTACACTA TGTGCTGTG

40

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCAGGTACC TTAAACATG CAGTTCATAC ATTTGAC

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATAGGATCC GCCATCATGA GCGTAGTCTG GGACGTCGTA TGGGTAAAGT TACACTATGT

60

TGCTGTG

67

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCAGGTACC TTAAACATG CAGTTCATAC ATTTGAC

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gln Leu Leu Cys Tyr Phe Val Ile Leu Phe Val Gly Ile Ala Pro  
1 5 10 15  
Trp Ser Ser Leu Ala Asn Asp Asp Gly Cys Asn Glu Val Val Cys Gly  
20 25 30  
Ser Val Val Ser Lys Cys Leu Ile Thr Gln Ser Cys Gln Cys Lys Leu  
35 40 45  
Asn Asp Cys His Cys Cys Lys Asp Cys Leu Asn Cys Leu Gly Glu Leu  
50 55 60  
Tyr Ile Glu Cys Cys Gly Cys Leu Asp Met Cys Pro Lys His Lys Asp  
65 70 75 80  
Val Leu Pro Ser Leu Thr Pro Arg Ser Glu Ile Gly Asp Ile Glu Gly  
85 90 95  
Val Pro Glu Leu Phe Asp Thr Leu Thr Ala Glu Asp Asp Glu Gly Trp  
100 105 110  
Ser Thr Ile Arg Phe Ser Met Arg Ala Gly Phe Lys Gln Arg Val Ala  
115 120 125  
Gln Gly Gly Ala Ser Gly Asp Ala Gly Asn Gly Asn Gly Asn Gly Asn  
130 135 140  
Ala Gly Ser Ala Gly Val Thr Leu Cys Thr Val Ile Tyr Asn Ser Cys  
145 150 155 160  
Ile Arg Ala Asn Lys Cys Arg Gln Gln Cys Glu Ser Met Gly Ala Ser  
165 170 175  
Ser Tyr Arg Trp Phe His Asp Gly Cys Cys Glu Cys Val Gly Glu Asn  
180 185 190  
Cys Leu Asn Tyr Gly Ile Asn Glu Ser Arg Cys Arg Gly Cys  
195 200 205